

SEQUENCE LISTING

<110> Cahoon, Rebecca E
Miao, Gou-Hau
Powell, Wayne

<120> Plant Farnesyltransferases

<130> BB-1240

<140> 09/786,675

<141>

<150> 60/099,521

<151> 1998-09-08

<160> 23

<170> Microsoft Office 97

<210> 1

<211> 1426

<212> DNA

<213> Zea mays

<400> 1

```
gcacgagaca gcgcaattac ttaagctatt tgtattcgga tctgatccaa ccctgggtggt 60
cagctggact catcgcccat ggagcacact aagtcaggcc ccagcagttg gccagaactg 120
gccgacgtgg tgccggtgcc gcaggacgat gggcctagcc ctgtggtgtc catcgccctat 180
cgagatgact ttcgtgaggt catggattac ttccgcgccc tctacctcac cggtgagcga 240
agccctcgcg ctctccgcct caccgcccag gccatcgagc tcaaccccgg caactacact 300
gtctggcatt tccggcgccct tattctggag tcaactagatt ttgatttact agaggagatg 360
aaatattgtcg aaaaaattgc tgaatgcaat ccaaaaaatt accaaatctg gcaccataag 420
agatggcttg ctgagaaatt aggacctggg attgcaaaca aagagcatga attcacaatg 480
aagatacttg ctattgatgc aaaaaattat catgcttggt ctcataggca gtgggttctt 540
caagcgttgg ggggatggga gactgaatta gaatactgtg accacttact taaggaagac 600
gtcttcaata attcagcttg gaatcagaga tactttgtta taacaagatc accatttctt 660
gggtggccttg cggcaatgcg tgattcagaa gtagactaca caattgaagc tattctagca 720
aacgctcaga atgaaagccc ctggaggtag ctcaagggtc tatacaaggg tgagaataac 780
ctgctagtag aggacgagcg catctctgct gtttgtttca aggtcctgaa gaatgattgg 840
acttggtgat ttgctttgag tttgctgctc gatcttctct gcactgggtt gcagccttca 900
gatgaactta ggtccactct tgaacaata aggagctccc atcctgaaac cgcggatgat 960
gatcctgcag ccgctgtttg ctgtatcctg cagaaatgtg atccccctgc ggtaaattat 1020
tggtcttggt tcaaggacac tctttctcag atctcatgac ttcacatggg ttcacccctt 1080
gtccgcgctg gtccgggctc tgtgagatag acatgtttta gatagtttca ttggacaccc 1140
aaacagagcg gacagagtgt atggctgcta ccttctccgt gactgaaagc agtgcttgta 1200
acgattttgt ttagtaaaat ttgtgagtgt tactgtccca aacaacacct tatgcaacca 1260
tatttgaaata tttcacatgt aagcttgaat ccagggtgtg ttgttaatgt attacaattg 1320
ccatgggagc ctaaatagaga cccataatca cttccactag agtcggaaga ccgtgtcgag 1380
cagttcactc atatggtcac ttaaagcaaa aaaaaaaaaa aaaaaa 1426
```

<210> 2

<211> 326

<212> PRT

<213> Zea mays

<400> 2

```
Met Glu His Thr Lys Ser Gly Pro Ser Ser Trp Pro Glu Leu Ala Asp
  1                      5                      10                      15
```

```
Val Val Pro Val Pro Gln Asp Asp Gly Pro Ser Pro Val Val Ser Ile
```

20					25					30					
Ala	Tyr	Arg	Asp	Asp	Phe	Arg	Glu	Val	Met	Asp	Tyr	Phe	Arg	Ala	Leu
		35					40					45			
Tyr	Leu	Thr	Gly	Glu	Arg	Ser	Pro	Arg	Ala	Leu	Arg	Leu	Thr	Ala	Glu
	50					55					60				
Ala	Ile	Glu	Leu	Asn	Pro	Gly	Asn	Tyr	Thr	Val	Trp	His	Phe	Arg	Arg
65					70					75					80
Leu	Ile	Leu	Glu	Ser	Leu	Asp	Phe	Asp	Leu	Leu	Glu	Glu	Met	Lys	Phe
				85					90					95	
Val	Glu	Lys	Ile	Ala	Glu	Cys	Asn	Pro	Lys	Asn	Tyr	Gln	Ile	Trp	His
			100					105					110		
His	Lys	Arg	Trp	Leu	Ala	Glu	Lys	Leu	Gly	Pro	Gly	Ile	Ala	Asn	Lys
		115					120					125			
Glu	His	Glu	Phe	Thr	Met	Lys	Ile	Leu	Ala	Ile	Asp	Ala	Lys	Asn	Tyr
	130					135					140				
His	Ala	Trp	Ser	His	Arg	Gln	Trp	Val	Leu	Gln	Ala	Leu	Gly	Gly	Trp
145					150					155					160
Glu	Thr	Glu	Leu	Glu	Tyr	Cys	Asp	His	Leu	Leu	Lys	Glu	Asp	Val	Phe
				165					170					175	
Asn	Asn	Ser	Ala	Trp	Asn	Gln	Arg	Tyr	Phe	Val	Ile	Thr	Arg	Ser	Pro
			180					185					190		
Phe	Leu	Gly	Gly	Leu	Ala	Ala	Met	Arg	Asp	Ser	Glu	Val	Asp	Tyr	Thr
		195					200					205			
Ile	Glu	Ala	Ile	Leu	Ala	Asn	Ala	Gln	Asn	Glu	Ser	Pro	Trp	Arg	Tyr
	210					215					220				
Leu	Lys	Gly	Leu	Tyr	Lys	Gly	Glu	Asn	Asn	Leu	Leu	Val	Glu	Asp	Glu
225					230					235					240
Arg	Ile	Ser	Ala	Val	Cys	Phe	Lys	Val	Leu	Lys	Asn	Asp	Trp	Thr	Cys
				245					250					255	
Val	Phe	Ala	Leu	Ser	Leu	Leu	Leu	Asp	Leu	Leu	Cys	Thr	Gly	Leu	Gln
			260					265					270		
Pro	Ser	Asp	Glu	Leu	Arg	Ser	Thr	Leu	Glu	Thr	Ile	Arg	Ser	Ser	His
		275					280					285			
Pro	Glu	Thr	Ala	Asp	Asp	Asp	Pro	Ala	Ala	Ala	Val	Cys	Cys	Ile	Leu
	290					295					300				
Gln	Lys	Cys	Asp	Pro	Leu	Arg	Val	Asn	Tyr	Trp	Ser	Trp	Phe	Lys	Asp
305					310					315					320
Thr	Leu	Ser	Gln	Ile	Ser										
				325											

<210> 3

<211> 1218

<212> DNA
 <213> Oryza sativa

<400> 3
 gcacgaggtt ctaacgccgc cgccgccgcc gccgtctccg cagaatctga tcgatggcgc 60
 cgctcgtcgac gtcgtcggag ggtgcctccg acgagtgggt gccacccagc cggcgggccgg 120
 agctggcgga cgtgggtccc gtgacgcagg acgacgggcc ccaccccggt gtggccatcg 180
 cctaccggga cgagttccgc gaggtcatgg actacttccg cgccctctac ttcgccggcg 240
 agcgcagcgt ccgcgccctc cacctcaccc ccgaggatcat cgacctaat cccggcaact 300
 acacgggtgtg gcattttagg cgtcttggtc tagaggcact ggatgctgat ctgcgtgagg 360
 aaatggattt tgtggaccga attgctgaat gtaacccaaa aaattatcaa atctggcatc 420
 acaagagatg gcttgccggag aaattaggac cagatattgc aaataaagag cacgaattta 480
 caaggaagat actttctatg gatgctaaaa attaccatgc ttggtctcat aggcagtggg 540
 ttcttcaagc actgggtgga tgggagactg aactacagta ttgcaaccag ctgcttgagg 600
 aagacgtctt caataattca gcttggaatc agagatacct tgtaataaca agttcaccac 660
 ttcttgaggg ccttgccagca atgcgtgact cggaagtgga ttacacagtt ggggctattc 720
 tggctaacc tcagaatgaa agcccctgga gatacctcaa aggcctgtac aagggtgaaa 780
 ataacttgct gatggctgat gagcgcattc ctgatgtttg tctcaaggtc ctgaaacatg 840
 attcgacctg cgtatttgct ttgagcttgc tgctcgatct tcttcaaatt gggtttacaac 900
 cttcagatga actcaaagga actatcgaag caataaagaa ctctgatcct gaagcagatg 960
 aagcagtaga tgctgatctt gcgactgcaa tctgctcaat attgcagaga tgtgatcccc 1020
 tgcggataaa ttactgggtc tggtagagga ccactatttc ttctcaaacc tgaagcatgc 1080
 agtggcctcc atgaggtcat aatggagata tcttctatct tcgtgtgatt ctgggcgttg 1140
 aggtgcctag ctacatttgt tatgaacttt ccttggggcat aactgatcac tgatattact 1200
 ccaatattgt gttctaaa 1218

<210> 4
 <211> 339
 <212> PRT
 <213> Oryza sativa

<400> 4
 Met Ala Pro Ser Ser Thr Ser Ser Glu Gly Ala Ser Asp Glu Trp Leu
 1 5 10 15
 Pro Pro Ser Arg Arg Pro Glu Leu Ala Asp Val Val Pro Val Thr Gln
 20 25 30
 Asp Asp Gly Pro His Pro Val Val Ala Ile Ala Tyr Arg Asp Glu Phe
 35 40 45
 Arg Glu Val Met Asp Tyr Phe Arg Ala Leu Tyr Phe Ala Gly Glu Arg
 50 55 60
 Ser Val Arg Ala Leu His Leu Thr Ala Glu Val Ile Asp Leu Asn Pro
 65 70 75 80
 Gly Asn Tyr Thr Val Trp His Phe Arg Arg Leu Val Leu Glu Ala Leu
 85 90 95
 Asp Ala Asp Leu Arg Glu Glu Met Asp Phe Val Asp Arg Ile Ala Glu
 100 105 110
 Cys Asn Pro Lys Asn Tyr Gln Ile Trp His His Lys Arg Trp Leu Ala
 115 120 125
 Glu Lys Leu Gly Pro Asp Ile Ala Asn Lys Glu His Glu Phe Thr Arg
 130 135 140
 Lys Ile Leu Ser Met Asp Ala Lys Asn Tyr His Ala Trp Ser His Arg
 145 150 155 160

Gln Trp Val Leu Gln Ala Leu Gly Gly Trp Glu Thr Glu Leu Gln Tyr
 165 170 175
 Cys Asn Gln Leu Leu Glu Glu Asp Val Phe Asn Asn Ser Ala Trp Asn
 180 185 190
 Gln Arg Tyr Leu Val Ile Thr Ser Ser Pro Leu Leu Gly Gly Leu Ala
 195 200 205
 Ala Met Arg Asp Ser Glu Val Asp Tyr Thr Val Gly Ala Ile Leu Ala
 210 215 220
 Asn Pro Gln Asn Glu Ser Pro Trp Arg Tyr Leu Lys Gly Leu Tyr Lys
 225 230 235 240
 Gly Glu Asn Asn Leu Leu Met Ala Asp Glu Arg Ile Ser Asp Val Cys
 245 250 255
 Leu Lys Val Leu Lys His Asp Ser Thr Cys Val Phe Ala Leu Ser Leu
 260 265 270
 Leu Leu Asp Leu Leu Gln Ile Gly Leu Gln Pro Ser Asp Glu Leu Lys
 275 280 285
 Gly Thr Ile Glu Ala Ile Lys Asn Ser Asp Pro Glu Ala Asp Glu Ala
 290 295 300
 Val Asp Ala Asp Leu Ala Thr Ala Ile Cys Ser Ile Leu Gln Arg Cys
 305 310 315 320
 Asp Pro Leu Arg Ile Asn Tyr Trp Ser Trp Tyr Arg Thr Thr Ile Ser
 325 330 335

Ser Gln Thr

<210> 5
 <211> 1261
 <212> DNA
 <213> Glycine max

<400> 5
 gcacgaggat taacgaagga tggaaatctgg gtctagcgaa ggagaagagg tgcagcaacg 60
 cgtgccgttg agggagagag tggagtgggc agatgttact ccggttcctc aaaacgacgg 120
 ccctaaccct gtcgttccga tccagtacac tgaagagttt tccgaagtta tggattactt 180
 tcgcgccgtt tacctcaccg atgaacgctc ccctcgcgcc ctgctctca cagccgaagc 240
 cgttcaattc aactccggca actacactgt gtggcatttc cgacggttgt tacttgagtc 300
 gctaaaagtc gacttgaacg atgaactgga ttttgtggag cgtatggccg ctggaaattc 360
 taaaaattat cagatgtggc atcatagacg atgggttgcc gagaagttag gtcctgaagc 420
 tagaaacaat gagctcgagt tcacaaaaaa gatactgtcc gttgatgcc aacattatca 480
 tgcattggtc catagacagt gggctcttca aacactagga ggatgggaag atgaacttaa 540
 ttattgcaca gaactactta aagaagacat ttttaacaat tctgcttgga atcagagata 600
 ttttgtcata acaaggcttc ctttcttggg gggcctaaaa gctatgagag agtctgaagt 660
 gctttacacc attgaagcca ttatagccta ccctgaaaaat gaaagctcgt ggagatatct 720
 acgaggactt tataaagggtg aaactacttc atgggttaa atgatcctcaag tttcttcagt 780
 atgcttaaa attttgagaa ctaagagcaa ctacgtgttt gctcttagca ctattttaga 840
 tcttatatgc tttgggtatc aaccaaata agacattaga gatgccattg acgccttaaa 900
 gaccgcagat atggataaac aagattttaga tgatgatgag aaaggggaac aacaaaattt 960
 aaatatagca cgaaatatct gttctatcct aaaacaagtt gatccaatta gaaccaacta 1020
 ttggatttgg cgcaagagca gacttcctct atcagcttag taaccaaggt aattaaaggg 1080

```

caactctgtg ttatgtgtaa cctagtttat tgaaactgga tttttattta ttattatttt 1140
ttatgttgtc atgtatctgt ttgtgcaaat ttatcttttt gtcatgccat tactggcatt 1200
tgagtgtgaa gattgaaagc catgcagaat aagaaattta agtttttttt tccgttgaaa 1260
a                                                                                   1261

```

```

<210> 6
<211> 346
<212> PRT
<213> Glycine max

```

```

<400> 6
Met Glu Ser Gly Ser Ser Glu Gly Glu Glu Val Gln Gln Arg Val Pro
  1              5              10              15

Leu Arg Glu Arg Val Glu Trp Ser Asp Val Thr Pro Val Pro Gln Asn
              20              25              30

Asp Gly Pro Asn Pro Val Val Pro Ile Gln Tyr Thr Glu Glu Phe Ser
      35              40              45

Glu Val Met Asp Tyr Phe Arg Ala Val Tyr Leu Thr Asp Glu Arg Ser
      50              55              60

Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly
      65              70              75              80

Asn Tyr Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys
              85              90              95

Val Asp Leu Asn Asp Glu Leu Asp Phe Val Glu Arg Met Ala Ala Gly
      100              105              110

Asn Ser Lys Asn Tyr Gln Met Trp His His Arg Arg Trp Val Ala Glu
      115              120              125

Lys Leu Gly Pro Glu Ala Arg Asn Asn Glu Leu Glu Phe Thr Lys Lys
      130              135              140

Ile Leu Ser Val Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln
      145              150              155              160

Trp Ala Leu Gln Thr Leu Gly Gly Trp Glu Asp Glu Leu Asn Tyr Cys
              165              170              175

Thr Glu Leu Leu Lys Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln
      180              185              190

Arg Tyr Phe Val Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala
      195              200              205

Met Arg Glu Ser Glu Val Leu Tyr Thr Ile Glu Ala Ile Ile Ala Tyr
      210              215              220

Pro Glu Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly
      225              230              235              240

Glu Thr Thr Ser Trp Val Asn Asp Pro Gln Val Ser Ser Val Cys Leu
      245              250              255

Lys Ile Leu Arg Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile
      260              265              270

```

Leu Asp Leu Ile Cys Phe Gly Tyr Gln Pro Asn Glu Asp Ile Arg Asp
 275 280 285
 Ala Ile Asp Ala Leu Lys Thr Ala Asp Met Asp Lys Gln Asp Leu Asp
 290 295 300
 Asp Asp Glu Lys Gly Glu Gln Gln Asn Leu Asn Ile Ala Arg Asn Ile
 305 310 315 320
 Cys Ser Ile Leu Lys Gln Val Asp Pro Ile Arg Thr Asn Tyr Trp Ile
 325 330 335
 Trp Arg Lys Ser Arg Leu Pro Leu Ser Ala
 340 345

<210> 7
 <211> 1333
 <212> DNA
 <213> Glycine max

<400> 7
 gcacgagctt gcgtgtggag tgaagaagat taacgaagga tggaaatctgg gtctagcgaa 60
 ggagaagagg tgcagcaacg cgtgccgttg agggagagag tggagtggtc agatgttact 120
 ccggttcctc aaaacgacgg ccctaaccct gtcgttccga tccagtacac tgaagagttt 180
 tccgaagtta tggattactt tcgcgcggtt tacctcaccg atgaacgctc ccctcgcgcc 240
 ctcgctctca cagccgaagc cgttcaattc aactccggca actacactgt gtggcatttc 300
 cgacggttgt tacttgagtc gctaaaagtc gacttgaacg atgaactgga gtttgtggag 360
 cgtatggccg ctggaaattc taaaaattat cagatgtggt gtgatgctct gctctgctct 420
 ttcttccata ctttgcacat tagacgatgg gttgccgaga agttaggtcc tgaagctaga 480
 aacaatgagc tcgagttcac caaaaagata ctgtccggtg atgccaaaca ttatcatgca 540
 tgggtctcata gacagtgggc tcttcaaaca ctaggaggat gggaagatga acttaattat 600
 tgcacagaac tacttaaaga agacattttt aacaattctg cttggaatca gagatatttt 660
 gtcataacaa ggtctccttt cttggggggc ctaaaagcta tgagagagtc tgaagtgtt 720
 tacaccattg aagccattat agcctaccct gaaaatgaaa gctcgtggag atatctacga 780
 ggactttata aaggtgaaac tacttcatgg gttaatgata ctcaagtttc ttcagtatgc 840
 ttaaagattt tgagaactaa gagcaactac gtgtttgctc ttagcactat tttagatcct 900
 atatgctttg gttatcaacc aaatgaagac attagagatg ccattgacgc cttaaagacc 960
 gcagatatgg ataaacaaga tttagatgat gatgagaaag gggaacaaca aaatttaaat 1020
 atagcacgaa atatttggtc taccctaaaa caagttgatc caattagaac caactatttg 1080
 atttggcgca agagcagact tcctctatca gcttagtaac caaagtaatt aaagggcaac 1140
 tctgtgttat gtgtaaccta gtttattgaa actggatggt tattttattat tattttttat 1200
 gttgtcatgt atctgtttgt gcaaatttat ctttttgtca tgccattact ggcatttgag 1260
 tgtaaggatt gaaagccatg cagaataaga aatttaagtt tttttttccg ttgaaaaaaa 1320
 aaaaaaaaaa aaa 1333

<210> 8
 <211> 358
 <212> PRT
 <213> Glycine max

<400> 8
 Met Glu Ser Gly Ser Ser Glu Gly Glu Glu Val Gln Gln Arg Val Pro
 1 5 10 15
 Leu Arg Glu Arg Val Glu Trp Ser Asp Val Thr Pro Val Pro Gln Asn
 20 25 30
 Asp Gly Pro Asn Pro Val Val Pro Ile Gln Tyr Thr Glu Glu Phe Ser
 35 40 45

Glu Val Met Asp Tyr Phe Arg Ala Val Tyr Leu Thr Asp Glu Arg Ser
 50 55 60
 Pro Arg Ala Leu Ala Leu Thr Ala Glu Ala Val Gln Phe Asn Ser Gly
 65 70 75 80
 Asn Tyr Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys
 85 90 95
 Val Asp Leu Asn Asp Glu Leu Glu Phe Val Glu Arg Met Ala Ala Gly
 100 105 110
 Asn Ser Lys Asn Tyr Gln Met Trp Cys Asp Ala Leu Leu Cys Ser Phe
 115 120 125
 Phe His Thr Leu His His Arg Arg Trp Val Ala Glu Lys Leu Gly Pro
 130 135 140
 Glu Ala Arg Asn Asn Glu Leu Glu Phe Thr Lys Lys Ile Leu Ser Val
 145 150 155 160
 Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln Trp Ala Leu Gln
 165 170 175
 Thr Leu Gly Gly Trp Glu Asp Glu Leu Asn Tyr Cys Thr Glu Leu Leu
 180 185 190
 Lys Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Phe Val
 195 200 205
 Ile Thr Arg Ser Pro Phe Leu Gly Gly Leu Lys Ala Met Arg Glu Ser
 210 215 220
 Glu Val Leu Tyr Thr Ile Glu Ala Ile Ile Ala Tyr Pro Glu Asn Glu
 225 230 235 240
 Ser Ser Trp Arg Tyr Leu Arg Gly Leu Tyr Lys Gly Glu Thr Thr Ser
 245 250 255
 Trp Val Asn Asp Pro Gln Val Ser Ser Val Cys Leu Lys Ile Leu Arg
 260 265 270
 Thr Lys Ser Asn Tyr Val Phe Ala Leu Ser Thr Ile Leu Asp Leu Ile
 275 280 285
 Cys Phe Gly Tyr Gln Pro Asn Glu Asp Ile Arg Asp Ala Ile Asp Ala
 290 295 300
 Leu Lys Thr Ala Asp Met Asp Lys Gln Asp Leu Asp Asp Asp Glu Lys
 305 310 315 320
 Gly Glu Gln Gln Asn Leu Asn Ile Ala Arg Asn Ile Cys Ser Ile Leu
 325 330 335
 Lys Gln Val Asp Pro Ile Arg Thr Asn Tyr Trp Ile Trp Arg Lys Ser
 340 345 350
 Arg Leu Pro Leu Ser Ala
 355

<210> 9

<211> 1339
 <212> DNA
 <213> Triticum aestivum

<400> 9
 cggacgtggc gccgctgccg caggccgacg ggccctgccc cgtcgtctcc atcgcttacc 60
 gcggcgactt ccgcgaggtc atggactact tccgcgccct ctacgccgcc ggcgagcgca 120
 gccccgcgc cctccgcctc accgccgacg ccatccacct caaccccgcc aactacactg 180
 tatggcattt caggcgcgtt gttctagagg cactggatgc tgatttattg ctagaaatgc 240
 attttgtgga ccaaattgct gaatctaata caaaaaatta ccaagtctgg catcacaaga 300
 gatggcttgc tgagaaaata ggaccagatg ctgcaaatag tgaacatgac ttcacaagga 360
 agatacttgc tatggatgct aaaaactacc atgcttggtc ccataggcag tgggttcttc 420
 aagcattggg tggatgggag agtgaactgc agtactgcaa ccagcttctt gaggaagatg 480
 tcttcaataa ctacagcttg aatcagagat acctgtggtt aacacgatca ccaattcttg 540
 ggggccttgc ggcaatgcgc gactcagaag tagattacac agttgaggcc attatggtga 600
 accctcagaa tgaaagcccc tggagatacc tcagagggtt atataaggat gataacaatt 660
 tgctgggtggc tgataatcgc atttctgatg cttgcctcaa ggtcctgaat aaggattgga 720
 catgcgtatt tgctttgagc ttctgtcttg atcttcttcg catgggtttg cagccttcga 780
 atgaacttaa aggaaccatc gaagcaatgg agaactctga tcctgaaacg ggacatgctg 840
 atattgcagt agctgtctgc tcaatcctgc agaaatgtga tcccctgcgg ataaactact 900
 ggtcatggta ccagaccact ctttcttctt agacatctga aaattcagct gaagacagtt 960
 ttagcagcat gatgtaaact caatcgaagg ggttgacgca gtgtatgaaa aacctttcct 1020
 gtgatcttgg tcgaggagcaa tttgtactga ttttactggg aaaaatcaat caatgacagc 1080
 atgcccaca atgtcttgtg tgaatatgtt actgcctgat attcacatgt tagcagaatg 1140
 agaataacca atcaaactcc aacgagcaga ttgttacagt aacggccact ggtggtgtga 1200
 aaatcctgaa atctgcttca gtcactttgc cttgtttaca gttgagctctg ttgttgtgat 1260
 ctgtacctaa tgcattgaca caatcatcaa attattagtt tttgtaccaa tgagtattcg 1320
 atgaaaaaaaa aaaaaaaaaa 1339

<210> 10
 <211> 309
 <212> PRT
 <213> Triticum aestivum

<400> 10
 Asp Val Ala Pro Leu Pro Gln Ala Asp Gly Pro Cys Pro Val Val Ser
 1 5 10 15
 Ile Ala Tyr Arg Gly Asp Phe Arg Glu Val Met Asp Tyr Phe Arg Ala
 20 25 30
 Leu Tyr Ala Ala Gly Glu Arg Ser Pro Arg Ala Leu Arg Leu Thr Ala
 35 40 45
 Asp Ala Ile His Leu Asn Pro Gly Asn Tyr Thr Val Trp His Phe Arg
 50 55 60
 Arg Val Val Leu Glu Ala Leu Asp Ala Asp Leu Leu Leu Glu Met His
 65 70 75 80
 Phe Val Asp Gln Ile Ala Glu Ser Asn Pro Lys Asn Tyr Gln Val Trp
 85 90 95
 His His Lys Arg Trp Leu Ala Glu Lys Ile Gly Pro Asp Ala Ala Asn
 100 105 110
 Ser Glu His Asp Phe Thr Arg Lys Ile Leu Ala Met Asp Ala Lys Asn
 115 120 125
 Tyr His Ala Trp Ser His Arg Gln Trp Val Leu Gln Ala Leu Gly Gly
 130 135 140

Trp Glu Ser Glu Leu Gln Tyr Cys Asn Gln Leu Leu Glu Glu Asp Val
 145 150 155 160
 Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Leu Val Val Thr Arg Ser
 165 170 175
 Pro Ile Leu Gly Gly Leu Ala Ala Met Arg Asp Ser Glu Val Asp Tyr
 180 185 190
 Thr Val Glu Ala Ile Met Val Asn Pro Gln Asn Glu Ser Pro Trp Arg
 195 200 205
 Tyr Leu Arg Gly Leu Tyr Lys Asp Asp Asn Asn Leu Leu Val Ala Asp
 210 215 220
 Asn Arg Ile Ser Asp Ala Cys Leu Lys Val Leu Asn Lys Asp Trp Thr
 225 230 235 240
 Cys Val Phe Ala Leu Ser Phe Leu Leu Asp Leu Leu Arg Met Gly Leu
 245 250 255
 Gln Pro Ser Asn Glu Leu Lys Gly Thr Ile Glu Ala Met Glu Asn Ser
 260 265 270
 Asp Pro Glu Thr Gly His Ala Asp Ile Ala Val Ala Val Cys Ser Ile
 275 280 285
 Leu Gln Lys Cys Asp Pro Leu Arg Ile Asn Tyr Trp Ser Trp Tyr Gln
 290 295 300
 Thr Thr Leu Ser Ser
 305

<210> 11
 <211> 1359
 <212> DNA
 <213> Zea mays

<400> 11
 atggaccctt ccccgagctc gacgccgccc accggagacg acccggcagc ggcggcggat 60
 cccgacctac cgaggctcac ggtgacgcag gtggagcaga tgaagggtga ggccaggggt 120
 ggcgacatct accgctccct cttcggggcc gcgcccaaca cgaaatccat catgctagag 180
 ctgtggcggtg atcagcatat cgagtatctg acgcctgggc tgaggcatat gggaccagcc 240
 ttctcatgttc tagatgccaa tcgcccttgg ctatgctact ggatgggttca tccacttgct 300
 ttgctgggatg aagcacttga tgatgatctt gagaatgata tcatagactt cttagctcga 360
 tgtcaggata aagatgggtg atatagtggg ggacctggac agttgcctca cctagctacg 420
 acttatgctg ctgtaaatac acttgtgaca atagggagcg aaagagcatt gtcatacaatc 480
 aataggggca acctgtacaa ttttatgctg cagatgaaag atgtatcagg tgctttcaga 540
 atgcatgatg gtggcgaaat tgatgtccgt gcttcctaca ccgctatatc gggtggccagc 600
 cttgtgaata ttcttgattt taaactggca aaagggtgtg gcgactacat agcaagatgt 660
 caaacttatg aagtggtgat tgctggggag ccttatgctg aagcacatgg tgggtataca 720
 ttctgtggat tggctgcttt gatcctgctt aatgaggcag agaaagttga cttgcctagt 780
 ttgatgggct ggggtggcttt tcgtcaagga gtggaatgcy gatttcaagg acgaactaat 840
 aaattgggtg atgggttgcta ctctttttgg caggagctg ccattgcttt cacacaaaag 900
 ttaattacga ttgttgataa gcaattgaag tcctcgtatt cctgcaaaag gccatcagga 960
 gaggatgcct gcagaccag ttcatatggg tgcaccgcga aaaagtcttc ctctgctgtg 1020
 gactatgcga agtttggtt tgattttata caacagagca accaaattgg cccactcttc 1080
 cataacattg ccctgcaaca atacatccta ctttgttctc aggtactaga gggaggcttg 1140
 agggataagc ctggaaagaa cagagatcac tatcattcat gctactgcct cagtggcctc 1200
 gcagtttagcc agtacagtgc catgactgat actggttcgt gccattacc tcagcatgtg 1260

cttggaccgt actctaattt gctggagcca atccatccac tctacaatgt tgtcctagat 1320
aagtaccata cagcctatga gttcttctca gaagagtga 1359

<210> 12
<211> 452
<212> PRT
<213> Zea mays

<400> 12
Met Asp Pro Ser Pro Gln Ser Thr Pro Pro Thr Gly Asp Asp Pro Ala
1 5 10 15
Ala Ala Ala Asp Pro Asp Leu Pro Arg Leu Thr Val Thr Gln Val Glu
20 25 30
Gln Met Lys Val Glu Ala Arg Val Gly Asp Ile Tyr Arg Ser Leu Phe
35 40 45
Gly Ala Ala Pro Asn Thr Lys Ser Ile Met Leu Glu Leu Trp Arg Asp
50 55 60
Gln His Ile Glu Tyr Leu Thr Pro Gly Leu Arg His Met Gly Pro Ala
65 70 75 80
Phe His Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Met Val
85 90 95
His Pro Leu Ala Leu Leu Asp Glu Ala Leu Asp Asp Asp Leu Glu Asn
100 105 110
Asp Ile Ile Asp Phe Leu Ala Arg Cys Gln Asp Lys Asp Gly Gly Tyr
115 120 125
Ser Gly Gly Pro Gly Gln Leu Pro His Leu Ala Thr Thr Tyr Ala Ala
130 135 140
Val Asn Thr Leu Val Thr Ile Gly Ser Glu Arg Ala Leu Ser Ser Ile
145 150 155 160
Asn Arg Gly Asn Leu Tyr Asn Phe Met Leu Gln Met Lys Asp Val Ser
165 170 175
Gly Ala Phe Arg Met His Asp Gly Gly Glu Ile Asp Val Arg Ala Ser
180 185 190
Tyr Thr Ala Ile Ser Val Ala Ser Leu Val Asn Ile Leu Asp Phe Lys
195 200 205
Leu Ala Lys Gly Val Gly Asp Tyr Ile Ala Arg Cys Gln Thr Tyr Glu
210 215 220
Gly Gly Ile Ala Gly Glu Pro Tyr Ala Glu Ala His Gly Gly Tyr Thr
225 230 235 240
Phe Cys Gly Leu Ala Ala Leu Ile Leu Leu Asn Glu Ala Glu Lys Val
245 250 255
Asp Leu Pro Ser Leu Ile Gly Trp Val Ala Phe Arg Gln Gly Val Glu
260 265 270
Cys Gly Phe Gln Gly Arg Thr Asn Lys Leu Val Asp Gly Cys Tyr Ser

275		280		285
Phe Trp Gln Gly Ala Ala Ile Ala Phe Thr Gln Lys Leu Ile Thr Ile				
290		295		300
Val Asp Lys Gln Leu Lys Ser Ser Tyr Ser Cys Lys Arg Pro Ser Gly				
305		310		315
Glu Asp Ala Cys Ser Thr Ser Ser Tyr Gly Cys Thr Ala Lys Lys Ser				
		325		330
Ser Ser Ala Val Asp Tyr Ala Lys Phe Gly Phe Asp Phe Ile Gln Gln				
		340		345
Ser Asn Gln Ile Gly Pro Leu Phe His Asn Ile Ala Leu Gln Gln Tyr				
		355		360
Ile Leu Leu Cys Ser Gln Val Leu Glu Gly Gly Leu Arg Asp Lys Pro				
		370		375
Gly Lys Asn Arg Asp His Tyr His Ser Cys Tyr Cys Leu Ser Gly Leu				
385		390		395
Ala Val Ser Gln Tyr Ser Ala Met Thr Asp Thr Gly Ser Cys Pro Leu				
		405		410
Pro Gln His Val Leu Gly Pro Tyr Ser Asn Leu Leu Glu Pro Ile His				
		420		425
Pro Leu Tyr Asn Val Val Leu Asp Lys Tyr His Thr Ala Tyr Glu Phe				
		435		440
Phe Ser Glu Glu				
450				

<210> 13
 <211> 1031
 <212> DNA
 <213> Oryza sativa

<400> 13
 gcacgagggc gtagccgcct ttcgggtgaga tccccgcggc tgcagcgagc tgcaggccg 60
 ccgccttccg cgccgccgac caccgcgccc atggaccccc cctcgccgcc gccgccgccg 120
 ccatacctc ctgctgctgc tgagggcggg ccggcagcgg atagccaggc cgctgagctg 180
 ccccggtga ctgtgacgca ggtggagcag atgaaggtgg aggcgaaggt gggcgaaatc 240
 taccgcgtcc tcttcggcaa cgcgccaac gccaatccc tcatgttaga gctgtggcgt 300
 gagcagcatg ttgagtattt gacgagaggg ctgaaacatc ttggaccaag cttccatgtg 360
 ctcgatgcca atcgacctg gctgtgctac tggattattc atgcacttgc tctgttggat 420
 gaaatacctg acgatgttga ggatgatatt gtggacttct tatctcgatg tcaggacaaa 480
 gatggtggtt atggcggagg acctggacag ttgcctcatc tcgctacaac ttatgctgct 540
 gtaaatacac ttgtaactat agggagtga agggcactat catcggtaaa cagggacaac 600
 ctgtacaagt tcatgcttcg gatgaaagat acatcgggag ctttcagaat gcatgatggt 660
 ggtgaaatag atgttcgtgc tagctatact gcaatatcgg ttgccagcct tgtgaacatt 720
 cttgatggtg aactagcaaa aggtgttggg aattacataa caaggtgtca aacctatgaa 780
 ggtggcattg ctggggaacc gtatgctgaa gctcatgggtg ggtacacttt ttgtgggctg 840
 gctacgatga tcctgcttaa cgaagtggac aaacttgatt tggctagctt gattggctgg 900
 gtggcatttc gccaaaggag ggaatgtgga tttcaaggac gaactaataa attggttgat 960
 ggttgctact ccttttggca gggagctgct cttgctttaa ctgttcaccg cgtggcgccg 1020
 actgccaac g 1031

<210> 14

<211> 313
 <212> PRT
 <213> Oryza sativa

<400> 14

Met	Asp	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Tyr	Pro	Pro	Ala	Ala		
1				5					10					15			
Ala	Glu	Gly	Gly	Pro	Ala	Ala	Asp	Ser	Gln	Ala	Ala	Glu	Leu	Pro	Arg		
			20					25					30				
Leu	Thr	Val	Thr	Gln	Val	Glu	Gln	Met	Lys	Val	Glu	Ala	Lys	Val	Gly		
		35					40					45					
Glu	Ile	Tyr	Arg	Val	Leu	Phe	Gly	Asn	Ala	Pro	Asn	Ala	Asn	Ser	Leu		
	50					55					60						
Met	Leu	Glu	Leu	Trp	Arg	Glu	Gln	His	Val	Glu	Tyr	Leu	Thr	Arg	Gly		
65					70					75					80		
Leu	Lys	His	Leu	Gly	Pro	Ser	Phe	His	Val	Leu	Asp	Ala	Asn	Arg	Pro		
			85						90					95			
Trp	Leu	Cys	Tyr	Trp	Ile	Ile	His	Ala	Leu	Ala	Leu	Leu	Asp	Glu	Ile		
		100					105						110				
Pro	Asp	Asp	Val	Glu	Asp	Asp	Ile	Val	Asp	Phe	Leu	Ser	Arg	Cys	Gln		
	115						120					125					
Asp	Lys	Asp	Gly	Gly	Tyr	Gly	Gly	Gly	Pro	Gly	Gln	Leu	Pro	His	Leu		
	130					135					140						
Ala	Thr	Thr	Tyr	Ala	Ala	Val	Asn	Thr	Leu	Val	Thr	Ile	Gly	Ser	Glu		
145				150					155						160		
Arg	Ala	Leu	Ser	Ser	Val	Asn	Arg	Asp	Asn	Leu	Tyr	Lys	Phe	Met	Leu		
			165					170						175			
Arg	Met	Lys	Asp	Thr	Ser	Gly	Ala	Phe	Arg	Met	His	Asp	Gly	Gly	Glu		
		180					185					190					
Ile	Asp	Val	Arg	Ala	Ser	Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Leu	Val		
	195						200					205					
Asn	Ile	Leu	Asp	Gly	Glu	Leu	Ala	Lys	Gly	Val	Gly	Asn	Tyr	Ile	Thr		
	210					215					220						
Arg	Cys	Gln	Thr	Tyr	Glu	Gly	Gly	Ile	Ala	Gly	Glu	Pro	Tyr	Ala	Glu		
225					230					235					240		
Ala	His	Gly	Gly	Tyr	Thr	Phe	Cys	Gly	Leu	Ala	Thr	Met	Ile	Leu	Leu		
			245					250					255				
Asn	Glu	Val	Asp	Lys	Leu	Asp	Leu	Ala	Ser	Leu	Ile	Gly	Trp	Val	Ala		
		260					265						270				
Phe	Arg	Gln	Gly	Val	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu		
	275						280					285					
Val	Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Ala	Ala	Leu	Ala	Leu	Thr		
	290					295					300						

Val His Arg Val Ala Pro Thr Ala Lys
305 310

<210> 15
<211> 1504
<212> DNA
<213> Glycine max

<400> 15
gcacgaggac aaatccgccg ccgccgccgc cgtgtccgac ggtgagtcaa cgtgagcaat 60
ggatggtaga gtcgcaggtg tttcagattt accaactctt cgccaccatt cctcgcaacg 120
cccaaaccct catgttggag cttcaacgcg ataatcacat gcagtatgtc tccaaaggcc 180
ttcgccatct cagttccgca ttttccgttt tggacgctaa tcgaccctgg ctctgctact 240
ggatcttcca ctccattgct ttgtcgggag aatccgctga tgatgaactc gaagataacg 300
ctatcgattt tcttaaccgt tgccaggatc cgaatggtgg atatgccggg ggaccaggcc 360
agatgcctca tattgccaca acttatgctg ctgttaattc acttattact ttgggtggtg 420
agaaatccct ggcattcaatt aatagagata aactgtatgg gtttctgcgg cggatgaagc 480
aaccaaatgg tggattcagg atgcatgatg aagggtgaaat tgatgttcga gcttgctaca 540
ctgccatttc tgttgcaagt gttttgaaca ttttggatga tgagctgac cagaatggtg 600
gagactacat tataagctgt caaacatatg aggggtggcat tgctgggtgag cctggttctg 660
aggctcatgg tgggtacacc ttttgtggat tagctacaat gattctgatt ggtgagggtta 720
atcacttgga tctgcctcga ttagttgact ggggtggtatt ccgacaaggc aaggaatgtg 780
gattccaggg gagaacaaat aaactggtgg atggatgcta ttccttttgg caggagggtg 840
ctgttgctct attgcaaaga ttatcttcta ttatcaacaa acagatggaa gagacatcac 900
agatttttgc ggtatcttat gtatctgaag caaaagaaaag tttggatgga acctctagtc 960
atgcaacatg ccgtggtgag catgaaggca ccagtgaatc cagttcatct gattttaaaa 1020
atattgccta taaatttatt aatgagtggg gagcacaaga accacttttt cacagtattg 1080
ctttacagca atatatcttc ttatgtgcac aggagcaaga ggggtggactg agagacaaac 1140
cgggtaaacg tagagatcat tatcacacat gttactgttt aagtggactc tcattgtgcc 1200
agtatagttg gtcaaagcac ccagattctc caccactgcc taatctagta ttaggccct 1260
actctaactc cttagaacca atccaccccc tctttaatgt tgtcttgga cgatatcgtg 1320
aagctcatga attcttcttt actgagtcgt gaccactggt ttagctacc aacaacttta 1380
tttgtataat gtaaaaataaa ttcattggaa catataaatg taaaacagca ttggattaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaa 1504

<210> 16
<211> 429
<212> PRT
<213> Glycine max

<400> 16
Met Val Glu Ser Gln Val Phe Gln Ile Tyr Gln Leu Phe Ala Thr Ile
1 5 10 15
Pro Arg Asn Ala Gln Thr Leu Met Leu Glu Leu Gln Arg Asp Asn His
20 25 30
Met Gln Tyr Val Ser Lys Gly Leu Arg His Leu Ser Ser Ala Phe Ser
35 40 45
Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Ile Phe His Ser
50 55 60
Ile Ala Leu Ser Gly Glu Ser Val Asp Asp Glu Leu Glu Asp Asn Ala
65 70 75 80
Ile Asp Phe Leu Asn Arg Cys Gln Asp Pro Asn Gly Gly Tyr Ala Gly
85 90 95

Gly Pro Gly Gln Met Pro His Ile Ala Thr Thr Tyr Ala Ala Val Asn
 100 105 110
 Ser Leu Ile Thr Leu Gly Gly Glu Lys Ser Leu Ala Ser Ile Asn Arg
 115 120 125
 Asp Lys Leu Tyr Gly Phe Leu Arg Arg Met Lys Gln Pro Asn Gly Gly
 130 135 140
 Phe Arg Met His Asp Glu Gly Glu Ile Asp Val Arg Ala Cys Tyr Thr
 145 150 155 160
 Ala Ile Ser Val Ala Ser Val Leu Asn Ile Leu Asp Asp Glu Leu Ile
 165 170 175
 Gln Asn Val Gly Asp Tyr Ile Ile Ser Cys Gln Thr Tyr Glu Gly Gly
 180 185 190
 Ile Ala Gly Glu Pro Gly Ser Glu Ala His Gly Gly Tyr Thr Phe Cys
 195 200 205
 Gly Leu Ala Thr Met Ile Leu Ile Gly Glu Val Asn His Leu Asp Leu
 210 215 220
 Pro Arg Leu Val Asp Trp Val Val Phe Arg Gln Gly Lys Glu Cys Gly
 225 230 235 240
 Phe Gln Gly Arg Thr Asn Lys Leu Val Asp Gly Cys Tyr Ser Phe Trp
 245 250 255
 Gln Gly Gly Ala Val Ala Leu Leu Gln Arg Leu Ser Ser Ile Ile Asn
 260 265 270
 Lys Gln Met Glu Glu Thr Ser Gln Ile Phe Ala Val Ser Tyr Val Ser
 275 280 285
 Glu Ala Lys Glu Ser Leu Asp Gly Thr Ser Ser His Ala Thr Cys Arg
 290 295 300
 Gly Glu His Glu Gly Thr Ser Glu Ser Ser Ser Ser Asp Phe Lys Asn
 305 310 315 320
 Ile Ala Tyr Lys Phe Ile Asn Glu Trp Arg Ala Gln Glu Pro Leu Phe
 325 330 335
 His Ser Ile Ala Leu Gln Gln Tyr Ile Leu Leu Cys Ala Gln Glu Gln
 340 345 350
 Glu Gly Gly Leu Arg Asp Lys Pro Gly Lys Arg Arg Asp His Tyr His
 355 360 365
 Thr Cys Tyr Cys Leu Ser Gly Leu Ser Leu Cys Gln Tyr Ser Trp Ser
 370 375 380
 Lys His Pro Asp Ser Pro Pro Leu Pro Asn Leu Val Leu Gly Pro Tyr
 385 390 395 400
 Ser Asn Leu Leu Glu Pro Ile His Pro Leu Phe Asn Val Val Leu Gly
 405 410 415
 Arg Tyr Arg Glu Ala His Glu Phe Phe Phe Thr Glu Ser

420

425

<210> 17
 <211> 533
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (499)
 <223> n = A, C, G or T

<220>
 <221> unsure
 <222> (525)
 <223> n = A, C, G or T

<400> 17
 gagagagata cgaatccggc ggcgggcgcca ccgtgtccga cgggtgagtca acggggaccag 60
 tggatggtag agtcgcaggt gtttcagatt taccaactct ttgccaccat tcctggcagc 120
 gcccaaaacc tcatgttaga gctgcaacgc gataatcaca tgcagtatct ctccaaaggc 180
 ctacgccatc tcagttccgc gttttctgtc ttggacgcta atcgaccctg gctctgttac 240
 tggatcttcc attccattgc tttgctggga gaatccgtcg acgacgaact cgaagataac 300
 actatcgatt ttcttaaccg ttgccaggat ccgaatggtg gatatgctgg gggaccaggc 360
 cagatgcctc acattgccac aacatatgct gcagttaata cacttattac tttgggtggt 420
 cagaaatcct ggcatcaatt aataggtgag ataaactgta tgggtttctg cggcggatga 480
 agcaatcaaa tggggggant caagatgcac gatgaaagga gaaanttgat gtc 533

<210> 18
 <211> 141
 <212> PRT
 <213> Glycine max

<400> 18
 Asp Thr Asn Pro Ala Ala Ala Pro Pro Cys Pro Thr Val Ser Gln Arg
 1 5 10 15
 Asp Gln Trp Met Val Glu Ser Gln Val Phe Gln Ile Tyr Gln Leu Phe
 20 25 30
 Ala Thr Ile Pro Gly Ser Ala Gln Asn Leu Met Leu Glu Leu Gln Arg
 35 40 45
 Asp Asn His Met Gln Tyr Leu Ser Lys Gly Leu Arg His Leu Ser Ser
 50 55 60
 Ala Phe Ser Val Leu Asp Ala Asn Arg Pro Trp Leu Cys Tyr Trp Ile
 65 70 75 80
 Phe His Ser Ile Ala Leu Leu Gly Glu Ser Val Asp Asp Glu Leu Glu
 85 90 95
 Asp Asn Thr Ile Asp Phe Leu Asn Arg Cys Gln Asp Pro Asn Gly Gly
 100 105 110
 Tyr Ala Gly Gly Pro Gly Gln Met Pro His Ile Ala Thr Thr Tyr Ala
 115 120 125
 Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Gln Lys Ser
 130 135 140

<210> 19
 <211> 333
 <212> PRT
 <213> Pisum sativum

<400> 19
 Met Ala Gly Asn Ile Glu Val Glu Glu Asp Asp Arg Val Pro Leu Arg
 1 5 10 15
 Leu Arg Pro Glu Trp Ser Asp Val Thr Pro Ile Pro Gln Asp Asp Gly
 20 25 30
 Pro Ser Pro Val Val Pro Ile Asn Tyr Ser Glu Glu Phe Ser Glu Val
 35 40 45
 Met Asp Tyr Phe Arg Ala Val Tyr Phe Ala Lys Glu Leu Ser Ser Arg
 50 55 60
 Ala Leu Ala Leu Thr Ala Glu Ala Ile Gly Leu Asn Ala Gly Asn Tyr
 65 70 75 80
 Thr Val Trp His Phe Arg Arg Leu Leu Leu Glu Ser Leu Lys Val Asp
 85 90 95
 Leu His Val Glu Arg Glu Phe Val Glu Arg Val Ala Ser Gly Asn Ser
 100 105 110
 Lys Asn Tyr Gln Ile Trp His His Arg Arg Trp Val Ala Glu Lys Leu
 115 120 125
 Gly Pro Glu Ala Arg Asn Ser Glu Leu Glu Phe Thr Lys Lys Ile Leu
 130 135 140
 Ser Val Asp Ala Lys His Tyr His Ala Trp Ser His Arg Gln Trp Val
 145 150 155 160
 Leu Gln Asn Leu Gly Gly Trp Glu Asp Glu Leu Ser Tyr Cys Ser Glu
 165 170 175
 Leu Leu Ala Glu Asp Ile Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr
 180 185 190
 Phe Val Ile Thr Arg Ser Pro Val Leu Gly Gly Leu Lys Ala Met Arg
 195 200 205
 Glu Ser Glu Val Leu Phe Thr Val Glu Ala Ile Ile Ser Tyr Pro Glu
 210 215 220
 Asn Glu Ser Ser Trp Arg Tyr Leu Arg Gly Leu Phe Lys Asp Glu Ser
 225 230 235 240
 Thr Leu Tyr Val Asn Asp Ala Gln Val Ser Ser Leu Cys Leu Lys Ile
 245 250 255
 Leu Lys Thr Lys Ser Asn Tyr Leu Phe Ala Leu Ser Thr Leu Leu Asp
 260 265 270
 Leu Ser Ala Ser Val Ile Gln Pro Asn Glu Asp Phe Arg Asp Ala Ile
 275 280 285
 Glu Ala Leu Arg Leu Gln Ile Leu Ile Lys Gln Asp Ser Asp Ile Ala

290 295 300
 Ile Thr Ile Cys Ser Ile Leu Glu Gln Val Asp Pro Ile Arg Val Asn
 305 310 315 320
 Tyr Trp Val Trp Arg Lys Ser Arg Leu Pro Gln Ala Ala
 325 330

 <210> 20
 <211> 326
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 20
 Met Asn Phe Asp Glu Thr Val Pro Leu Ser Gln Arg Leu Glu Trp Ser
 1 5 10 15
 Asp Val Val Pro Leu Thr Gln Asp Asp Gly Pro Asn Pro Val Val Pro
 20 25 30
 Ile Ala Tyr Lys Glu Glu Phe Arg Glu Thr Met Asp Tyr Phe Arg Ala
 35 40 45
 Ile Tyr Phe Ser Asp Glu Arg Ser Pro Arg Ala Leu Arg Leu Thr Glu
 50 55 60
 Glu Thr Leu Leu Leu Asn Ser Gly Asn Tyr Thr Val Trp His Phe Arg
 65 70 75 80
 Arg Leu Val Leu Glu Ala Leu Asn His Asp Leu Phe Glu Glu Leu Glu
 85 90 95
 Phe Ile Glu Arg Ile Ala Glu Asp Asn Ser Lys Asn Tyr Gln Leu Trp
 100 105 110
 His His Arg Arg Trp Val Ala Glu Lys Leu Gly Pro Asp Val Ala Gly
 115 120 125
 Arg Glu Leu Glu Phe Thr Arg Arg Val Leu Ser Leu Asp Ala Lys His
 130 135 140
 Tyr His Ala Trp Ser His Arg Gln Trp Thr Leu Arg Ala Leu Gly Gly
 145 150 155 160
 Trp Glu Asp Glu Leu Asp Tyr Cys His Glu Leu Leu Glu Ala Asp Val
 165 170 175
 Phe Asn Asn Ser Ala Trp Asn Gln Arg Tyr Tyr Val Ile Thr Gln Ser
 180 185 190
 Pro Leu Leu Gly Gly Leu Glu Ala Met Arg Glu Ser Glu Val Ser Tyr
 195 200 205
 Thr Ile Lys Ala Ile Leu Thr Asn Pro Ala Asn Glu Ser Ser Trp Arg
 210 215 220
 Tyr Leu Lys Ala Leu Tyr Lys Asp Asp Lys Glu Ser Trp Ile Ser Asp
 225 230 235 240
 Pro Ser Val Ser Ser Val Cys Leu Asn Val Leu Ser Arg Thr Asp Cys
 245 250 255

Phe His Gly Phe Ala Leu Ser Thr Leu Leu Asp Leu Leu Cys Asp Gly
 260 265 270
 Leu Arg Pro Thr Asn Glu His Lys Asp Ser Val Arg Ala Leu Ala Asn
 275 280 285
 Glu Glu Pro Glu Thr Asn Leu Ala Asn Leu Val Cys Thr Ile Leu Gly
 290 295 300
 Arg Val Asp Pro Ile Arg Ala Asn Tyr Trp Ala Trp Arg Lys Ser Lys
 305 310 315 320
 Ile Thr Val Ala Ala Ile
 325

<210> 21
 <211> 470
 <212> PRT
 <213> Lycopersicon esculentum

<400> 21
 Met Glu Ser Arg Lys Val Thr Lys Thr Leu Glu Asp Gln Trp Val Val
 1 5 10 15
 Glu Arg Arg Val Arg Glu Ile Tyr Asp Tyr Phe Tyr Ser Ile Ser Pro
 20 25 30
 Asn Ser Pro Ser Asp Leu Ile Glu Ile Glu Arg Asp Lys His Phe Gly
 35 40 45
 Tyr Leu Ser Gln Gly Leu Arg Lys Leu Gly Pro Ser Phe Ser Val Leu
 50 55 60
 Asp Ala Ser Arg Pro Trp Leu Cys Tyr Trp Thr Leu His Ser Ile Ala
 65 70 75 80
 Leu Leu Gly Glu Ser Ile Gly Gly Lys Leu Glu Asn Asp Ala Ile Asp
 85 90 95
 Phe Leu Thr Arg Cys Gln Asp Lys Asp Gly Gly Tyr Gly Gly Gly Pro
 100 105 110
 Gly Gln Met Pro His Leu Ala Thr Thr Tyr Ala Ala Val Asn Ser Leu
 115 120 125
 Ile Thr Leu Gly Lys Pro Glu Ala Leu Ser Ser Ile Asn Arg Glu Lys
 130 135 140
 Leu Tyr Thr Phe Leu Leu Arg Met Lys Asp Ala Ser Gly Gly Phe Arg
 145 150 155 160
 Met His Asp Gly Gly Glu Val Asp Val Arg Ala Cys Tyr Thr Ala Ile
 165 170 175
 Ser Val Ala Asn Ile Leu Asn Ile Val Asp Asp Glu Leu Ile His Gly
 180 185 190
 Val Gly Asn Tyr Ile Leu Ser Cys Gln Thr Tyr Glu Gly Gly Ile Ala
 195 200 205

Gly Glu Pro Gly Ser Glu Ala His Gly Gly Tyr Thr Phe Cys Gly Leu
 210 215 220
 Ala Ala Met Ile Leu Ile Asn Glu Val Asp Arg Leu Asp Leu Pro Gly
 225 230 235 240
 Leu Ile Asp Trp Val Val Phe Arg Gln Gly Val Glu Gly Gly Phe Gln
 245 250 255
 Gly Arg Thr Asn Lys Leu Val Asp Gly Cys Tyr Ser Phe Trp Gln Gly
 260 265 270
 Ala Val Val Phe Leu Ile Gln Arg Leu Asn Leu Ile Val His Glu Gln
 275 280 285
 Leu Gly Leu Ser Asn Asp Leu Ser Thr Glu Ser Ala Asp Asp Ser Ser
 290 295 300
 Glu Ser Glu Leu Ser Asp Glu Glu Glu His Leu Glu Gly Ile Ser Ser
 305 310 315 320
 His Val Gln Asp Thr Phe Pro Leu Gly Gln Ala Gly Ala Cys Gln Glu
 325 330 335
 Asn Ala Ser His Ser Pro Lys Ile Ala Asp Thr Gly Tyr Glu Phe Ile
 340 345 350
 Asn Arg Pro Ile Ala Met Arg Pro Leu Phe Asp Ser Met Tyr Leu Gln
 355 360 365
 Gln Tyr Val Leu Leu Cys Ser Gln Ile Glu Val Gly Gly Phe Arg Asp
 370 375 380
 Lys Pro Gly Lys Gly Arg Asp Tyr Tyr His Thr Cys Tyr Cys Leu Ser
 385 390 395 400
 Gly Leu Ser Ile Ala Gln Tyr Ser Trp Thr Asp Glu Ala Asp Ser Thr
 405 410 415
 Pro Leu Pro Arg Asp Val Phe Gly Pro Tyr Ser Lys Cys Leu Leu Glu
 420 425 430
 Gln Val His Pro Leu Phe Asn Val Val Leu Asp Arg Tyr Tyr Glu Ala
 435 440 445
 Arg Glu Tyr Ser Gln Ala Cys Glu Thr Val Ser Pro Leu Ser Leu Ala
 450 455 460
 Pro Thr Phe Ser Glu Thr
 465 470

<210> 22
 <211> 419
 <212> PRT
 <213> Pisum sativum

<400> 22
 Met Glu Ala Ser Thr Ala Ala Glu Thr Pro Thr Pro Thr Val Ser Gln
 1 5 10 15

Arg Asp Gln Trp Ile Val Glu Ser Gln Val Phe His Ile Tyr Gln Leu

20					25					30					
Phe	Ala	Asn	Ile	Pro	Pro	Asn	Ala	Gln	Ser	Ile	Ile	Arg	Pro	Trp	Leu
		35					40					45			
Cys	Tyr	Trp	Ile	Ile	His	Ser	Ile	Ala	Leu	Leu	Gly	Glu	Ser	Ile	Asp
	50					55					60				
Asp	Asp	Leu	Glu	Asp	Asn	Thr	Val	Asp	Phe	Leu	Asn	Arg	Cys	Gln	Asp
	65					70					75				80
Pro	Asn	Gly	Gly	Tyr	Ala	Gly	Gly	Pro	Gly	Gln	Met	Pro	His	Leu	Ala
				85					90					95	
Thr	Thr	Tyr	Ala	Ala	Val	Asn	Thr	Leu	Ile	Thr	Leu	Gly	Gly	Glu	Lys
			100					105					110		
Ser	Leu	Ala	Ser	Ile	Asn	Arg	Asn	Lys	Leu	Tyr	Gly	Phe	Met	Arg	Arg
		115					120					125			
Met	Lys	Gln	Pro	Asn	Gly	Gly	Phe	Arg	Met	His	Asp	Glu	Gly	Glu	Ile
	130					135					140				
Asp	Val	Arg	Ala	Cys	Tyr	Thr	Ala	Ile	Ser	Val	Ala	Ser	Val	Leu	Asn
	145					150					155				160
Ile	Leu	Asp	Asp	Glu	Leu	Ile	Lys	Asn	Val	Gly	Asp	Phe	Ile	Leu	Ser
				165					170					175	
Cys	Gln	Thr	Tyr	Glu	Gly	Gly	Leu	Ala	Gly	Glu	Pro	Gly	Ser	Glu	Ala
			180					185					190		
His	Gly	Gly	Tyr	Thr	Phe	Cys	Gly	Leu	Ala	Ala	Met	Ile	Leu	Ile	Gly
		195					200					205			
Glu	Val	Asn	Arg	Leu	Asp	Leu	Pro	Arg	Leu	Leu	Asp	Trp	Val	Val	Phe
	210					215					220				
Arg	Gln	Gly	Lys	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val
	225					230					235				240
Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln
				245					250					255	
Arg	Leu	His	Ser	Ile	Ile	Asp	Glu	Gln	Met	Ala	Glu	Ala	Ser	Gln	Phe
			260					265					270		
Val	Thr	Val	Ser	Asp	Ala	Pro	Glu	Glu	Lys	Glu	Cys	Leu	Asp	Gly	Thr
		275					280					285			
Ser	Ser	His	Ala	Thr	Ser	His	Ile	Arg	His	Glu	Gly	Met	Asn	Glu	Ser
	290					295					300				
Cys	Ser	Ser	Asp	Val	Lys	Asn	Ile	Gly	Tyr	Asn	Phe	Ile	Ser	Glu	Trp
	305					310					315				320
Arg	Gln	Ser	Glu	Pro	Leu	Phe	His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile
				325					330					335	
Leu	Leu	Cys	Ser	Gln	Glu	Gln	Asp	Gly	Gly	Leu	Arg	Asp	Lys	Pro	Gly
			340					345					350		

Lys Arg Arg Asp His Tyr His Ser Cys Tyr Cys Leu Ser Gly Leu Ser
 355 360 365
 Leu Cys Gln Tyr Ser Trp Ser Lys Arg Pro Asp Ser Pro Pro Leu Pro
 370 375 380
 Lys Val Val Met Gly Pro Tyr Ser Asn Leu Leu Glu Pro Ile His Pro
 385 390 395 400
 Leu Phe Asn Val Val Leu Asp Arg Tyr Arg Glu Ala His Glu Phe Phe
 405 410 415
 Ser Gln Leu

<210> 23
 <211> 419
 <212> PRT
 <213> Pisum sativum

<400> 23
 Met Glu Ala Ser Thr Ala Ala Glu Thr Pro Thr Pro Thr Val Ser Gln
 1 5 10 15
 Arg Asp Gln Trp Ile Val Glu Ser Gln Val Phe His Ile Tyr Gln Leu
 20 25 30
 Phe Ala Asn Ile Pro Pro Asn Ala Gln Ser Ile Ile Arg Pro Trp Leu
 35 40 45
 Cys Tyr Trp Ile Ile His Ser Ile Ala Leu Leu Gly Glu Ser Ile Asp
 50 55 60
 Asp Asp Leu Glu Asp Asn Thr Val Asp Phe Leu Asn Arg Cys Gln Asp
 65 70 75 80
 Pro Asn Gly Gly Tyr Ala Gly Gly Pro Gly Gln Met Pro His Leu Ala
 85 90 95
 Thr Thr Tyr Ala Ala Val Asn Thr Leu Ile Thr Leu Gly Gly Glu Lys
 100 105 110
 Ser Leu Ala Ser Ile Asn Arg Asn Lys Leu Tyr Gly Phe Met Arg Arg
 115 120 125
 Met Lys Gln Pro Asn Gly Gly Phe Arg Met His Asp Glu Gly Glu Ile
 130 135 140
 Asp Val Arg Ala Cys Tyr Thr Ala Ile Ser Val Ala Ser Val Leu Asn
 145 150 155 160
 Ile Leu Asp Asp Glu Leu Ile Lys Asn Val Gly Asp Phe Ile Leu Ser
 165 170 175
 Cys Gln Thr Tyr Glu Gly Gly Leu Ala Gly Glu Pro Gly Ser Glu Ala
 180 185 190
 His Gly Gly Tyr Thr Phe Cys Gly Leu Ala Ala Met Ile Leu Ile Gly
 195 200 205

Glu	Val	Asn	Arg	Leu	Asp	Leu	Pro	Arg	Leu	Leu	Asp	Trp	Val	Val	Phe	210	215	220
Arg	Gln	Gly	Lys	Glu	Cys	Gly	Phe	Gln	Gly	Arg	Thr	Asn	Lys	Leu	Val	225	230	235
Asp	Gly	Cys	Tyr	Ser	Phe	Trp	Gln	Gly	Gly	Ala	Val	Ala	Leu	Leu	Gln	245	250	255
Arg	Leu	His	Ser	Ile	Ile	Asp	Glu	Gln	Met	Ala	Glu	Ala	Ser	Gln	Phe	260	265	270
Val	Thr	Val	Ser	Asp	Ala	Pro	Glu	Glu	Lys	Glu	Cys	Leu	Asp	Gly	Thr	275	280	285
Ser	Ser	His	Ala	Thr	Ser	His	Ile	Arg	His	Glu	Gly	Met	Asn	Glu	Ser	290	295	300
Cys	Ser	Ser	Asp	Val	Lys	Asn	Ile	Gly	Tyr	Asn	Phe	Ile	Ser	Glu	Trp	305	310	315
Arg	Gln	Ser	Glu	Pro	Leu	Phe	His	Ser	Ile	Ala	Leu	Gln	Gln	Tyr	Ile	325	330	335
Leu	Leu	Cys	Ser	Gln	Glu	Gln	Asp	Gly	Gly	Leu	Arg	Asp	Lys	Pro	Gly	340	345	350
Lys	Arg	Arg	Asp	His	Tyr	His	Ser	Cys	Tyr	Cys	Leu	Ser	Gly	Leu	Ser	355	360	365
Leu	Cys	Gln	Tyr	Ser	Trp	Ser	Lys	Arg	Pro	Asp	Ser	Pro	Pro	Leu	Pro	370	375	380
Lys	Val	Val	Met	Gly	Pro	Tyr	Ser	Asn	Leu	Leu	Glu	Pro	Ile	His	Pro	385	390	395
Leu	Phe	Asn	Val	Val	Leu	Asp	Arg	Tyr	Arg	Glu	Ala	His	Glu	Phe	Phe	405	410	415
Ser	Gln	Leu																